SEQUENCE LISTING

<110> Lye, Stephen
Dong, Xuesen

<120> METHODS AND COMPOSITIONS FOR MODULATING A STEROID RECEPTOR

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His Arg Arg Gly Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg
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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
115 120 125

Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
130 135 140

Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
145 150 155 160

Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
165 170 175

Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Pro Ala Ala Val Pro
180 185 190

Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
195 200 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
210 215 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
245 250 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
260 265 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
275 280 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
290 295 300

Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
305 310 315 320

Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
325 330 335

Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
340 345 350

Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr

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        355                 360                 365

His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
    370                 375                 380

Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
385                 390                 395                 400

Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
                405                 410                 415

Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
            420                 425                 430

Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
        435                 440                 445

Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
    450                 455                 460

Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
465                 470                 475                 480

Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
                485                 490                 495

Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
            500                 505                 510

Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
        515                 520                 525

Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
    530                 535                 540

Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
545                 550                 555                 560

Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
                565                 570                 575

Glu Met Met Ile Arg Gln Arg Glu Met Glu Glu Gln Met Arg Arg Gln
            580                 585                 590

Arg Glu Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg
        595                 600                 605

Asp Met Arg Met Gly Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
    610                 615                 620
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Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Gly Ile
625 630 635 640

Gly Tyr Glu Ala Asn Pro Gly Val Pro Pro Ala Thr Met Ser Gly Ser
645 650 655

Met Met Gly Ser Asp Met Arg Thr Glu Arg Phe Gly Gln Gly Gly Ala
660 665 670

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Ala Gly Tyr Gly Arg Gly Arg Glu Glu Tyr Glu Gly Pro Asn Lys Lys
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Pro Arg Phe
705

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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

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Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Thr Pro Pro Ala Ser
        115                 120                 125

Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
    130                 135                 140

Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
145                 150                 155                 160

Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
                165                 170                 175

Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Pro Ala Ala Val Pro
            180                 185                 190

Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
        195                 200                 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
    210                 215                 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro Arg Arg Gly Gly Gly Glu
225                 230                 235                 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
                245                 250                 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
            260                 265                 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
        275                 280                 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
    290                 295                 300

Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
305                 310                 315                 320

Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
                325                 330                 335

Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
            340                 345                 350

Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
        355                 360                 365
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His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
    370                 375                 380

Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
385                 390                 395                 400

Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
                405                 410                 415

Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
            420                 425                 430

Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
        435                 440                 445

Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
    450                 455                 460

Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Thr Arg Phe
465                 470                 475                 480

Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
                485                 490                 495

Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
            500                 505                 510

Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
        515                 520                 525

Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
    530                 535                 540

Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
545                 550                 555                 560

Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
                565                 570                 575

Glu Met Met Ile Arg Gln Arg Glu Met Glu Asp Gln Met Arg Arg Gln
            580                 585                 590

Arg Glu Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg
        595                 600                 605

Asp Met Arg Met Gly Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
    610                 615                 620

Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Gly Ile
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Gly Tyr Glu Ala Asn Pro Gly Val Pro Pro Ala Thr Met Ser Gly Ser
645 650 655

Met Met Gly Ser Asp Met Arg Thr Glu Arg Phe Gly Gln Gly Gly Ala
660 665 670

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Pro Arg Phe
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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
115 120 125

Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
130 135 140

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Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
145                 150                 155                 160

Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
                165                 170                 175

Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
            180                 185                 190

Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
        195                 200                 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
    210                 215                 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
225                 230                 235                 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
                245                 250                 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
            260                 265                 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
        275                 280                 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
    290                 295                 300

Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
305                 310                 315                 320

Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
                325                 330                 335

Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
            340                 345                 350

Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
        355                 360                 365

His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
    370                 375                 380

Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
385                 390                 395                 400
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Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
405 410 415

Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
420 425 430

Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
435 440 445

Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
450 455 460

Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
465 470 475 480

Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
485 490 495

Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
500 505 510

Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
515 520 525

Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
530 535 540

Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
545 550 555 560

Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
565 570 575

Glu Met Met Ile Arg Gln Arg Glu Met Glu Glu Gln Met Arg Arg Gln
580 585 590

Arg Glu Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg
595 600 605

Asp Met Arg Met Gly Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
610 615 620

Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Gly Ile
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Met Met Gly Ser Asp Met Val Arg Met Ile Asp Val Gly

660 665

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His Pro Gln Pro His Gln Gln Gln Gln Pro Pro Pro Pro Pro Gln Asp
20 25 30

Ser Ser Lys Pro Val Val Ala Gln Gly Pro Gly Pro Ala Pro Gly Val
35 40 45

Gly Ser Ala Pro Pro Ala Ser Ser Ser Ala Pro Pro Ala Thr Pro Pro
50 55 60

Thr Ser Gly Ala Pro Pro Gly Ser Gly Pro Gly Pro Thr Pro Thr Pro
65 70 75 80

Pro Pro Ala Val Thr Ser Ala Pro Pro Gly Ala Pro Pro Pro Thr Pro
85 90 95

Pro Ser Ser Gly Val Pro Thr Thr Pro Pro Gln Ala Gly Gly Pro Pro
100 105 110

Pro Pro Pro Ala Ala Val Pro Gly Pro Gly Pro Gly Pro Lys Gln Gly
115 120 125

Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro Lys
130 135 140

Pro Gly Gly Gly Pro Gly Leu Ser Thr Pro Gly Gly His Pro Lys Pro
145 150 155 160

Pro His Arg Gly Gly Gly Glu Pro Arg Gly Gly Arg Gln His His Pro
165 170 175

Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro Gly
180 185 190

Gly Arg Ser Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala Asn
195 200 205

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Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg Cys
    210                 215                 220

Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu Phe
225                 230                 235                 240

Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile Asn
                245                 250                 255

Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu Ala
            260                 265                 270

Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg Gln
        275                 280                 285

Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg Asn
    290                 295                 300

Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser Gln
305                 310                 315                 320

Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly Arg
                325                 330                 335

Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala Arg
            340                 345                 350

Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr Thr
        355                 360                 365

Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp Glu Asp
    370                 375                 380

Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys Glu
385                 390                 395                 400

Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr Glu
                405                 410                 415

Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln Arg
            420                 425                 430

Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu Ser
        435                 440                 445

Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg Gln
    450                 455                 460
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Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu His
465                 470                 475                 480

Asn Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu Glu
                485                 490                 495

Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu Met
            500                 505                 510

Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met Gly
        515                 520                 525

Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly Ala
    530                 535                 540

Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro Pro
545                 550                 555                 560

Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly Val Pro
                565                 570                 575

Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr Glu
            580                 585                 590

Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro Arg
        595                 600                 605

Gly Met Gly Pro Gly Thr Pro Ala Gly Tyr Gly Arg Gly Arg Glu Glu
    610                 615                 620

Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
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His Arg Arg Gly Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg
            20                  25                  30
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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
115 120 125

Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
130 135 140

Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
145 150 155 160

Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
165 170 175

Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Pro Ala Ala Val Pro
180 185 190

Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
195 200 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
210 215 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
245 250 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
260 265 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
275 280 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu

290 295 300

Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
305 310 315 320

Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
325 330 335

Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
340 345 350

Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
355 360 365

His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
370 375 380

Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
385 390 395 400

Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
405 410 415

Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
420 425 430

Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
435 440 445

Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
450 455 460

Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
465 470 475 480

Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
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Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
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Lys Asp Ala Lys Asp Lys Leu Lys Lys Lys Lys Lys Lys
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Leu Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly
        35                  40                  45

Arg Gln Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val
    50                  55                  60

Arg Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe
65                  70                  75                  80

Ser Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg
                85                  90                  95

Gly Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala
            100                 105                 110

Ala Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr
        115                 120                 125

Thr Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp
    130                 135                 140

Glu Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln
145                 150                 155                 160

Lys Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu
                165                 170                 175

Tyr Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln
            180                 185                 190

Gln Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu
        195                 200                 205

Glu Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu
    210                 215                 220

Arg Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu
225                 230                 235                 240
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Leu His Asn Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln
245 250 255

Glu Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg
260 265 270

Glu Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg
275 280 285

Met Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly
290 295 300

Gly Ala Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe
305 310 315 320

Pro Pro Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly
325 330 335

Val Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg
340 345 350

Thr Glu Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly
355 360 365

Pro Arg Gly Met Gly Pro Gly Thr Pro Ala Gly Tyr Gly Arg Gly Arg
370 375 380

Glu Glu Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
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Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
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Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
                85                  90                  95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
            100                 105                 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
        115                 120                 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
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Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145                 150                 155                 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
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Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
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Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
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Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
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Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225                 230                 235                 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys
                245                 250                 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
            260                 265                 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
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Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
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Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
            340                 345                 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
        355                 360                 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
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Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385                 390                 395                 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
                405                 410                 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
            420                 425                 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
        435                 440                 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
    450                 455                 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465                 470                 475                 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
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Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
            500                 505                 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
        515                 520                 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
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Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
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Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
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Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
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Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
        595                 600                 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
    610                 615                 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
625                 630                 635                 640

Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
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Pro Gln Pro Leu Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
            660                 665                 670

Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile
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Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
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Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln
705                 710                 715                 720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
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Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
            740                 745                 750

Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
        755                 760                 765

Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
    770                 775                 780

Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr
785                 790                 795                 800

Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu
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Glu Phe Leu Cys Met Lys Val Leu Leu Leu Leu Asn Thr Ile Pro Leu
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Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
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Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
850 855 860

Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
865 870 875 880

His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
885 890 895

Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
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Leu Phe His Lys Lys
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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

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Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
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Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
        115                 120                 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
    130                 135                 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145                 150                 155                 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
                165                 170                 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
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Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
        195                 200                 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
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Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225                 230                 235                 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
                245                 250                 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
            260                 265                 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
        275                 280                 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
    290                 295                 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305                 310                 315                 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
                325                 330                 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
            340                 345                 350
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Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
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Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
    370                 375                 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385                 390                 395                 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
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Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
            420                 425                 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
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Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
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Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465                 470                 475                 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
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Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
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Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
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Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
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Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545                 550                 555                 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
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Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
            580                 585                 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
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Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
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610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
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His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
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Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
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Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Arg Met Lys
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Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr Met Trp Gln Ile Pro Gln
690 695 700

Glu Phe Val Lys Leu Gln Val Ser Gln Glu Glu Phe Leu Cys Met Lys
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Val Leu Leu Leu Leu Asn Thr Ile Pro Leu Glu Gly Leu Arg Ser Gln
725 730 735

Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr Ile Arg Glu Leu Ile Lys
740 745 750

Ala Ile Gly Leu Arg Gln Lys Gly Val Val Ser Ser Ser Gln Arg Phe
755 760 765

Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu His Asp Leu Val Lys Gln
770 775 780

Leu His Leu Tyr Cys Leu Asn Thr Phe Ile Gln Ser Arg Ala Leu Ser
785 790 795 800

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        35                  40                  45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
    50                  55                  60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65                  70                  75                  80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
                85                  90                  95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
            100                 105                 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
        115                 120                 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
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Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145                 150                 155                 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
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Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
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Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
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Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
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Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225                 230                 235                 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
                245                 250                 255
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Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
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Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
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Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
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His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305                 310                 315                 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
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Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
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Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
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Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
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Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385                 390                 395                 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
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Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
            420                 425                 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
        435                 440                 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
    450                 455                 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465                 470                 475                 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
                485                 490                 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
            500                 505                 510
```

```
Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
        515                 520                 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
    530                 535                 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545                 550                 555                 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
                565                 570                 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
            580                 585                 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
        595                 600                 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
    610                 615                 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625                 630                 635                 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
                645                 650                 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
            660                 665                 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Asp Ser Phe Gly Arg
        675                 680                 685

Ala Thr Lys Ser Asn Pro Val
    690                 695
```

<210> 13
<211> 764
<212> PRT
<213> Homo sapiens

<300>
<308> BAC11011
<309> 2004-09-03
<313> (1)..(764)

<400> 13

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Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly
1               5                   10                  15

Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
```

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            20                  25                  30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
        35                  40                  45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
    50                  55                  60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65                  70                  75                  80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
                85                  90                  95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
            100                 105                 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
        115                 120                 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
    130                 135                 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145                 150                 155                 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
                165                 170                 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
            180                 185                 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
        195                 200                 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
    210                 215                 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225                 230                 235                 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
                245                 250                 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
            260                 265                 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
        275                 280                 285
```

```
Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
    290                 295                 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305                 310                 315                 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
                325                 330                 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
            340                 345                 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
        355                 360                 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
    370                 375                 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385                 390                 395                 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
                405                 410                 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
            420                 425                 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
        435                 440                 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
    450                 455                 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465                 470                 475                 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
                485                 490                 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
            500                 505                 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
        515                 520                 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
    530                 535                 540
```

```
Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545                 550                 555                 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
                565                 570                 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
            580                 585                 590

Arg Ala Met Glu Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val
        595                 600                 605

Val Arg Ala Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro
    610                 615                 620

Asn Glu Ser Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln
625                 630                 635                 640

Asp Ile Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser Ile Glu
                645                 650                 655

Pro Asp Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp Thr Ser
            660                 665                 670

Ser Ser Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Leu
        675                 680                 685

Ser Val Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn Leu His
    690                 695                 700

Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu Met
705                 710                 715                 720

Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln Met
                725                 730                 735

Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Ser His Arg Ser Leu
            740                 745                 750

Ser Ser Phe Lys Leu Ala Lys Lys Ser Ser Ser Val
        755                 760
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<210> 14
<211> 690
<212> PRT
<213> Homo sapiens

<300>
<308> BAC11012
<309> 2004-09-03

<313> (1)..(690)

<400> 14

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1               5                  10                  15

Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
            20                  25                  30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
        35                  40                  45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
    50                  55                  60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65                  70                  75                  80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
                85                  90                  95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
            100                 105                 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
        115                 120                 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
    130                 135                 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145                 150                 155                 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
                165                 170                 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
            180                 185                 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
        195                 200                 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
    210                 215                 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225                 230                 235                 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
```

```
                245                 250                 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
            260                 265                 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
        275                 280                 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
    290                 295                 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305                 310                 315                 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
                325                 330                 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
            340                 345                 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
        355                 360                 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
    370                 375                 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385                 390                 395                 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
                405                 410                 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
            420                 425                 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
        435                 440                 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
    450                 455                 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465                 470                 475                 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
                485                 490                 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
            500                 505                 510
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Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
        515                 520                 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
    530                 535                 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545                 550                 555                 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
                565                 570                 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
            580                 585                 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
        595                 600                 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
    610                 615                 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625                 630                 635                 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
                645                 650                 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
            660                 665                 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Ser Ile Val
        675                 680                 685

Thr Ser
    690
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<210> 15
<211> 803
<212> PRT
<213> Homo sapiens

<300>
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<309> 2004-09-03
<313> (1)..(803)

<400> 15

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            20                  25                  30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
        35                  40                  45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
    50                  55                  60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65                  70                  75                  80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
                85                  90                  95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
            100                 105                 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
        115                 120                 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
    130                 135                 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145                 150                 155                 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
                165                 170                 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
            180                 185                 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
        195                 200                 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
    210                 215                 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225                 230                 235                 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
                245                 250                 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
            260                 265                 270
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Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr

```
    530                 535                 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545                 550                 555                 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
                565                 570                 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
            580                 585                 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
        595                 600                 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
    610                 615                 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
625                 630                 635                 640

Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
                645                 650                 655

Pro Gln Pro Val Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
            660                 665                 670

Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile
        675                 680                 685

Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
    690                 695                 700

Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln
705                 710                 715                 720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
                725                 730                 735

Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
            740                 745                 750

Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
        755                 760                 765

Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
    770                 775                 780

Asn Glu Ser His Arg Ser Leu Ser Ser Phe Lys Leu Ala Lys Lys Ser
785                 790                 795                 800
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Ser Ser Val

<210> 16
<211> 14
<212> PRT
<213> Homo sapiens

<400> 16

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<210> 17
<211> 7
<212> DNA
<213> Homo sapiens

<400> 17
ctgagtc 7

<210> 18
<211> 13
<212> PRT
<213> Homo sapiens

<400> 18

Tyr Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys
1 5 10

<210> 19
<211> 12
<212> PRT
<213> Homo sapiens

<400> 19

Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala Arg
1 5 10

<210> 20
<211> 14
<212> PRT
<213> Homo sapiens

<400> 20

Phe Ala Gln His Gly Thr Glu Glu Tyr Glu Tyr Ser Gln Arg
1 5 10

<210> 21
<211> 699
<212> PRT
<213> Mus musculus

<300>

<308> NP_076092
<309> 2004-08-24
<313> (1)..(699)

<400> 21

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1               5                  10                  15

His Arg Arg Gly Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg
            20                  25                  30

Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
        35                  40                  45

Pro Gly Pro Gly Gly Pro Lys Pro Pro Leu Pro Pro Pro Pro Pro His
    50                  55                  60

Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln Gln Pro
65                  70                  75                  80

Pro Pro His Gln Gln Pro Pro Pro His Gln Pro Pro His Gln Gln Pro
                85                  90                  95

Pro Pro Pro Pro Gln Glu Ser Lys Pro Val Val Pro Gln Gly Pro Gly
            100                 105                 110

Ser Ala Pro Gly Val Ser Ser Ala Pro Pro Pro Ala Val Ser Ala Pro
        115                 120                 125

Pro Ala Asn Pro Pro Thr Thr Gly Ala Pro Pro Gly Pro Gly Pro Thr
    130                 135                 140

Pro Thr Pro Pro Pro Ala Val Pro Ser Thr Ala Pro Gly Pro Pro Pro
145                 150                 155                 160

Pro Ser Thr Pro Ser Ser Gly Val Ser Thr Thr Pro Pro Gln Thr Gly
                165                 170                 175

Gly Pro Pro Pro Pro Pro Ala Gly Gly Ala Gly Pro Gly Pro Lys Pro
            180                 185                 190

Gly Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro
        195                 200                 205

Lys Pro Gly Gly Gly Pro Gly Met Gly Ala Pro Gly Gly His Pro Lys
    210                 215                 220

Pro Pro His Arg Gly Gly Gly Glu Pro Arg Gly Gly Arg Gln His His
225                 230                 235                 240
```

Ala Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro
245 250 255

Gly Pro Arg Thr Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala
260 265 270

Asn Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg
275 280 285

Cys Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu
290 295 300

Phe Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile
305 310 315 320

Asn Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu
325 330 335

Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg
340 345 350

Gln Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg
355 360 365

Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser
370 375 380

Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly
385 390 395 400

Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala
405 410 415

Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr
420 425 430

Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp Glu
435 440 445

Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys
450 455 460

Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr
465 470 475 480

Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln
485 490 495

```
Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu
            500                 505                 510

Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg
        515                 520                 525

Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu
    530                 535                 540

His Ser Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu
545                 550                 555                 560

Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu
                565                 570                 575

Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met
            580                 585                 590

Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly
        595                 600                 605

Thr Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro
    610                 615                 620

Pro Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly Val
625                 630                 635                 640

Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr
                645                 650                 655

Glu Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro
            660                 665                 670

Arg Gly Met Gly Pro Gly Thr Pro Ala Gly Tyr Gly Arg Gly Arg Glu
        675                 680                 685

Glu Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
    690                 695

<210>  22
<211>  7
<212>  PRT
<213>  Homo sapiens

<400>  22

Val Arg Met Ile Asp Val Gly
1               5
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Sequence Listing

SEQ ID NO. 1

PSF Long Form PSF-A

P23246
707 aa linear
Splicing factor, proline-and glutamine-rich (Polypyrimidine tract-binding protein-associated splicing factor) (PTB-associated splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit).

NP_005057
splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

CAA50283
707 aa linear
PTB-associated splicing factor [Homo sapiens].

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 61 ppppphqqqq qpppqqpppq qppphqppph pqphqqqqpp pppqdsskpv vaqgpgpapg
121 vgsappasss appatpptsg appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 aggppppppaa vpgpgpgpkq gpgpggpkgg kmpggpkpgg gpglstpggh pkpphrggge
241 prggrqhhpp yhqqhhqgpp pggpggrsee kisdsegfka nlsllrrpge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvflltt tprpvivepl eqlddedglp eklaqknpmy qkeretpprf
481 aqhgtfeyey sqrwksldem ekqqreqvek nmkdakdkle semedayheh qanllrqdlm
541 rrqeelrrme elhnqemqkr kemqlrqeee rrrreeemmi rqremeeqmr rqreesysrm
601 gymdprerdm rmggggamnm gdpygsgggk fpplgggggi gyeanpgvpp atmsgsmmgs
661 dmrterfgqg gagpvgggqp rgmgpgtpag ygrgreeyeg pnkkprf
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SEQ ID NO. 2

AAH51192
707 aa linear
Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens).

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 61 ppppphqqqq qpppqqpppq qppphqppph pqphqqqqpp pppqdsskpv vaqgpgpapg
121 vgstppasss appatpptsg appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 aggppppppaa vpgpgpgpkq gpgpggpkgg kmpggpkpgg gpglstpggh pkpprrggge
241 prggrqhhpp yhqqhhqgpp pggpggrsee kisdsegfka nlsllrrpge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvflltt tprpvivepl eqlddedglp eklaqknpmy qkeretptrf
481 aqhgtfeyey sqrwksldem ekqqreqvek nmkdakdkle semedayheh qanllrqdlm
541 rrqeelrrme elhnqemqkr kemqlrqeee rrrreeemmi rqremedqmr rqreesysrm
601 gymdprerdm rmggggamnm gdpygsgggk fpplgggggi gyeanpgvpp atmsgsmmgs
661 dmrterfgqg gagpvgggqp rgmgpgtpag ygrgreeyeg pnkkprf
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SEQ ID NO. 3

Isoform short - PSP-F
669aa

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  1 msrdrfrsrg gggggfhrrg ggggrgglhd frspppgmgl nqnrgpmgpg pgqsgpkppi
 61 pppppphqqqq qpppqqpppq qppphqppph pqphqqqqpp pppqdsskpv vaqgpgpapg
121 vgsappasss appatpptsg appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 aggpppppaa vpgpgpgpkq gpgpggpkgg kmpggpkpgg gpglstpggh pkpphrggge
241 prggrqhhpp yhqqhhqgpp pggpggrsee kisdsegfka nlsllrrpge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvflltt tprpvivepl eqlddedglp eklaqknpmy qkeretpprf
481 aqhgtfeyey sqrwksldem ekqqreqvek nmkdakdkle semedayheh qanllrqdlm
541 rrqeelrrme elhnqemqkr kemqlrqeee rrrreeemmi rqremeeqmr rqreesysrm
601 gymdprerdm rmggggamnm gdpygsggqk fpplgggggi gyeanpgvpp atmsgsmmgs
661 dmvrmidvg
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SEQ ID NO. 4

AAH04534
634 aa linear
SFPQ protein [Homo sapiens].

```
  1 pqqpppqqpp phqppphpqp hqqqqppppp qdsskpvvaq gpgpapgvgs appasssapp
 61 atpptsgapp gsgpgptptp ppavtsappg appptppssg vpttppqagg pppppaavpg
121 pgpgpkqgpg pggpkggkmp ggpkpgggpg lstpgghpkp phrgggeprg grqhhppyhq
181 qhhqgpppgg pggrseekis dsegfkanls llrrpgekty tqrcrlfvgn lpaditedef
241 krlfakygep gevfinkgkg fgfiklesra laeiakaeld dtpmrgrqlr vrfathaaal
301 svrnlspyvs nelleeafsq fgpieravvi vddrgrstgk givefaskpa arkafercse
361 gvfllttttpr pvivepleql ddedglpekl aqknpmyqke retpprfaqh gtfeyeysqr
421 wksldemekq qreqveknmk dakdklesem edayhehqan llrqdlmrrq eelrrmeelh
481 nqemqkrkem qlrqeeerrr reeemmirqr emeeqmrrqr eesysrmgym dprerdmrmg
541 gggamnmgdp ygsggqkfpp lgggggigye anpgvppatm sgsmmgsdmr terfgqggag
601 pvggqgprgm gpgtpagygr greeyegpnk kprf
```

SEQ ID NO. 5

AAH27708
525 aa linear
SFPQ protein [Homo sapiens].

```
  1 msrdrfrsrg gggggfhrrg ggggrgglhd frspppgmgl nqnrgpmgpg pgqsgpkppi
 61 pppppphqqqq qpppqqpppq qppphqppph pqphqqqqpp pppqdsskpv vaqgpgpapg
121 vgsappasss appatpptsg appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 aggpppppaa vpgpgpgpkq gpgpggpkgg kmpggpkpgg gpglstpggh pkpphrggge
241 prggrqhhpp yhqqhhqgpp pggpggrsee kisdsegfka nlsllrrpge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvflltt tprpvivepl eqlddedglp eklaqknpmy qkeretpprf
481 aqhgtfeyey sqrwksldem ekqqreqvek nmkdakdklk kkkkk
```

SEQ ID. NO. 6

CAA34747
396 aa linear
DEFINITION myoblast antigen 24.1D5 (Homo sapiens).

```
  1 efkrlfakyg epgevfinkg kgfgfikles ralaeiakae lddtpmrgrq lrvrfathaa
 61 alsvrnlspy vsnelleeaf sqfgpierav vivddrgrst gkgivefask paarkaferc
121 segvfllttt prpviveple qlddedglpe klaqknpmyq keretpprfa qhgtfeyeys
181 qrwksldeme kqqreqvekn mkdakdkles emedayhehq anllrqdlmr rqeelrrmee
241 lhnqemqkrk emqlrqeeer rrreeemmir qremeeqmrr qreesysrmg ymdprerdmr
301 mggggamnmg dpygsggqkf pplgggggig yeanpgvppa tmsgsmmgsd mrterfgqgg
361 agpvggqgpr gmgpgtpagy grgreeyegp nkkprf
```

SEQ ID NO. 7

NM_005066
3071 bp mRNA linear
Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA.

X70944 S56626
3071 bp mRNA linear
H.sapiens mRNA for PTB-associated splicing factor.

```
   1 ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgtcttc ttcgcttttg
  61 cctcgaccgc cccttgacca cagacatgtc tcgggatcgg ttccggagtc gtggcggtgg
 121 cggtggtggc ttccacaggc gtggaggagg cggcggccgc ggcggcctcc acgacttccg
 181 ttctccgccg cccggcatgg gcctcaatca gaatcgcggc cccatgggtc ctggcccggg
 241 ccagagcggc cctaagcctc cgatcccgcc accgcctcca caccaacagc agcaacagcc
 301 accaccgcag cagccaccgc cgcagcagcc gccaccgcat cagccgccgc cgcatccaca
 361 gccgcatcag cagcagcagc cgccgccacc gccgcaggac tcttccaagc ccgtcgttgc
 421 tcagggaccc ggccccgctc ccggagtagg cagcgcacca ccagcctcca gctcggcccc
 481 gcccgccact ccaccaacct cgggggcccc gccagggtcc gggccaggcc cgactccgac
 541 cccgccgcct gcagtcacct cggcccctcc cggggcgccg ccacccaccc cgccaagcag
 601 cggggtccct accacacctc ctcaggccgg aggcccgccg cctccgcccg cggcagtccc
 661 gggcccgggt ccagggccta agcagggccc aggtccgggt ggtcccaaag gcggcaaaat
 721 gcctggcggg ccgaagccag gtggcggccc gggcctaagt acgcctggcg gccaccccaa
 781 gccgccgcat cgaggcggcg gggagccccg cgggggccgc cagcaccacc cgccctacca
 841 ccagcagcat caccaggggc ccccgcccgg cgggcccggc ggccgcagcg aggagaagat
 901 ctcggactcg gaggggttta aagccaattt gtctctcttg aggaggcctg gagagaaaac
 961 ttacacacag cgatgtcggt tgtttgttgg gaatctacct gctgatatca cggaggatga
1021 attcaaaaga ctatttgcta aatatggaga accaggagaa gtttttatca acaaaggcaa
1081 aggattcgga tttattaagc ttgaatctag agctttggct gaaattgcca aagccgaact
1141 ggatgataca cccatgagag gtagacagct tcgagttcgc tttgccacac atgctgctgc
1201 cctttctgtt cgtaatcttt caccttatgt ttccaatgaa ctgttggaag aagcctttag
1261 ccaatttggt cctattgaaa gggctgttgt aatagtggat gatcgtggaa gatctacagg
1321 gaaaggcatt gttgaatttg cttctaagcc agcagcaaga aaggcatttg aacgatgcag
1381 tgaaggtgtt ttcttactga cgacaactcc tcgtccagtc attgtggaac cacttgaaca
1441 actagatgat gaagatggtc ttcctgaaaa acttgcccag aagaatccaa tgtatcaaaa
1501 ggagagagaa acccctcctc gttttgccca gcatggcacg tttgagtacg aatattctca
1561 gcgatggaag tctttggatg aaatggaaaa acagcaaagg gaacaagttg aaaaaaacat
1621 gaaagatgca aaagacaaat tggaaagtga aatggaagat gcctatcatg aacatcaggc
1681 aaatcttttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca tggaagaact
```

```
1741 tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattg aggcaagagg aggaacgacg
1801 tagaagagag gaagagatga tgattcgtca acgtgagatg gaagaacaaa tgaggcgcca
1861 aagagaggaa agttacagcc gaatgggcta catggatcca cgggaaagag acatgcgaat
1921 gggtggcgga ggagcaatga acatgggaga tccctatggt tcaggaggcc agaaatttcc
1981 acctctagga ggtggtggtg gcataggtta tgaagctaat cctggcgttc caccagcaac
2041 catgagtggt tccatgatgg gaagtgacat gcgtactgag cgctttgggc agggaggtgc
2101 ggggcctgtg ggtggacagg gtcctagagg aatggggcct ggaactccag caggatatgg
2161 tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga tgtgatattt
2221 aggctttcat tccagtttgt tttgtttttt tgtttagata ccaatctttt aaattcttgc
2281 attttagtaa gaaagctatc tttttatgga tgttagcagt ttattgacct aatatttgta
2341 aatggtctgt ttgggcaggt aaaattatgt aatgcagtgt ttggaacagg agaatttttt
2401 tttccttttt atttctttat tttttctttt ttactgtata atgtccctca agtttatggc
2461 agtgtacctt gtgccactga atttccaaag tgtaccaatt ttttttttt tactgtgctt
2521 caaataaata gaaaaatagt tataatattg gatcttcaac tttgccattc atgcttctat
2581 gcatattagg ctacgtattc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
2641 tatgccattt ctgggaaatg catctggagg ctaagtattg ctttctacaa ataattgccc
2701 cctttgtttt aaaaagaaga aatgcatatt gaagtagttt gatgatttgt ttggcatata
2761 ggaagcacgc tggtgctaag tatttttaa atggttatgt aagcaaagct gaactgtaaa
2821 tcttcaggaa tatgtattaa gattgtggaa tgggtgtaag acaattggta gggggtgaaa
2881 gtgggtttga ttaaatggat cttttatggc cctatgatct atcctttact tgaaagcttt
2941 tgaaaagtgg aaaggtcatt ttgttgcatt tccccatttc ttgtttttaa aagaccaaca
3001 aatctcaagc cctataaatg gcttgtattg aacttttaca tttgaattaa agatgttaaa
3061 catgaaaaaa a
```

SEQ ID NO. 8

BC051192
2622 bp mRNA linear
Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated), mRNA (cDNA clone), complete cds.

```
   1 tctgtgtcat ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgtcttc
  61 ttcgcttttg cctcgaccgc cccttgacca cagacatgtc tcgggatcgg ttccggagtc
 121 gtggcggtgg cggtggtggc ttccacaggc gtggaggagg cggcggccgc ggcggcctcc
 181 acgacttccg ttctccgccg cccggcatgg gcctcaatca gaatcgcggc cccatgggtc
 241 ctggcccggg ccagagcggc cctaagcctc cgatcccgcc accgcctcca caccaacagc
 301 agcaacagcc accaccgcag cagccaccgc cgcagcagcc gccaccgcat cagccgccgc
 361 cgcatccaca gccgcatcag cagcagcagc cgccgccacc gccgcaggac tcttccaagc
 421 ccgtcgttgc tcagggaccc ggccccgctc ccggagtagg cagcacacca ccagcctcca
 481 gctcggcccc gcccgccact ccaccaacct cgggggcccc gccagggtcc gggccaggcc
 541 cgactccgac cccgccgcct gcagtcacct cggcccctcc cggggcgccg ccacccaccc
 601 cgccaagcag cggggtccct accacacctc ctcaggccgg aggcccgccg cctccgcccg
 661 cggcagtccc gggcccgggt ccagggccta agcagggccc aggtccgggt ggtcccaaag
 721 gcggcaaaat gcctggcggg ccgaagccag gtggcggccc gggcctaagt acgcctggcg
 781 gccaccccaa gccgccgcgt cgaggcggcg gggagccccg cgggggccgc cagcaccacc
 841 cgccctacca ccagcagcat caccaggggc ccccgcccgg cgggcccggc ggccgcagcg
 901 aggagaagat ctcggactcg gaggggttta aagccaattt gtctctcttg aggaggcctg
 961 gagagaaaac ttacacacag cgatgtcggt tgtttgttgg gaatctacct gctgatatca
1021 cggaggatga attcaaaaga ctatttgcta aatatggaga accaggagaa gtttttatca
1081 acaaaggcaa aggattcgga tttattaagc ttgaatctag agctttggct gaaattgcca
1141 aagccgaact ggatgataca cccatgagag gtagacagct tcgagttcgc tttgccacac
1201 atgctgctgc cctttctgtt cgtaatcttt caccttatgt ttccaatgaa ctgttggaag
1261 aagcctttag ccaatttggt cctattgaaa gggctgttgt aatagtggat gatcgtggaa
1321 gatctacagg gaaaggcatt gttgaatttg cttctaagcc agcagcaaga aaggcatttg
```

```
1381 aacgatgcag tgaaggtgtt ttcttactga cgacaactcc tcgtccagtc attgtggaac
1441 cacttgaaca actagatgat gaagatggtc ttcctgaaaa acttgcccag aagaatccaa
1501 tgtatcaaaa ggagagagaa acccctactc gttttgccca gcatggcacg tttgagtacg
1561 aatattctca gcgatggaag tctttggatg aaatggaaaa acagcaaagg gaacaagttg
1621 aaaaaaacat gaaagatgca aaagacaaat tggaaagtga aatggaagat gcctatcatg
1681 aacatcaggc aaatcttttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca
1741 tggaagaact tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattg aggcaagagg
1801 aggaacgacg tagaagagag gaagagatga tgattcgtca acgtgagatg gaagaccaaa
1861 tgaggcgcca aagagaggaa agttacagcc gaatgggcta catggatcca cgggaaagag
1921 acatgcgaat gggtggcgga ggagcaatga acatgggaga tccctatggt tcaggaggcc
1981 agaaatttcc acctctagga ggtggtggtg gcataggtta tgaagctaat cctggcgttc
2041 caccagcaac catgagtggt tccatgatgg gaagtgacat gcgtactgag cgctttgggc
2101 agggaggtgc ggggcctgtg ggtggacagg gtcctagagg aatggggcct ggaactccag
2161 caggatatgg tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga
2221 tgtgatattt aggctttcat tccagtttgt tttgtttttt tgtttagata ccaatctttt
2281 aaattcttgc attttagtaa gaaagctatc tttttatgga tgttagcagt ttattgacct
2341 aatatttgta aatggtctgt ttgggcaggt aaaattatgt aatgcagtgt ttggaacagg
2401 agaatttttt tttccttttt atttctttat tttttctttt ttactgtata atgtccctca
2461 agtttatggc agtgtacctt gtgccactga atttccaaag tgtaccaatt ttttttttt
2521 tactgtgctt caaataaata gaaaaatagt tataaaaaaa aaaaaaaaaa aaaaaaaaaa
2581 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
```

SEQ ID NO. 9

X16850
2021 bp mRNA linear
Human mRNA for myoblast cell surface antigen 24.1D5.

```
   1 gaattcaaaa gactatttgc taaatatgga gaaccaggag aagtttttat caacaaaggc
  61 aaaggattcg gatttattaa gcttgaatct agagctttgg ctgaaattgc caaagccgaa
 121 ctggatgata cacccatgag aggtagacag cttcgagttc gctttgccac acatgctgct
 181 gccctttctg ttcgtaatct ttcaccttat gtttccaatg aactgttgga agaagccttt
 241 agccaatttg gtcctattga aagggctgtt gtaatagtgg atgatcgtgg aagatctaca
 301 gggaaaggca ttgttgaatt tgcttctaag ccagcagcaa gaaaggcatt tgaacgatgc
 361 agtgaaggtg ttttcttact gacgacaact cctcgtccag tcattgtgga accacttgaa
 421 caactagatg atgaagatgg tcttcctgaa aaacttgccc agaagaatcc aatgtatcaa
 481 aaggagagag aaaccctcc tcgttttgcc cagcatggca cgtttgagta cgaatattct
 541 cagcgatgga agtctttgga tgaaatggaa aaacagcaaa gggaacaagt tgaaaaaaac
 601 atgaaagatg caaaagacaa attggaaagt gaaatggaag atgcctatca tgaacatcag
 661 gcaaatcttt tgcgccaaga tctgatgaga cgacaggaag aattaagacg catggaagaa
 721 cttcacaatc aagaaatgca gaaacgtaaa gaaatgcaat tgaggcaaga ggaggaacga
 781 cgtagaagag aggaagagat gatgattcgt caacgtgaga tggaagaaca aatgaggcgc
 841 caaagagagg aaagttacag ccgaatgggc tacatggatc cacgggaaag agacatgcga
 901 atgggtggcg gaggagcaat gaacatggga gatccctatg gttcaggagg ccagaaattt
 961 ccacctctag gaggtggtgg tggcataggt tatgaagcta atcctggcgt tccaccagca
1021 accatgagtg gttccatgat gggaagtgac atgcgtactg agcgctttgg gcagggaggt
1081 gcggggcctg tgggtggaca gggtcctaga ggaatggggc ctggaactcc agcaggatat
1141 ggtagaggga gagaagagta cgaaggccca aacaaaaaac cccgatttta gatgtgatat
1201 ttaggctttc attccagttt gttttgtttt tttgtttaga taccaatctt ttaaattctt
1261 gcattttagt aagaaagcta tctttttatg gatgttagca gtttattgac ctaatatttg
1321 taaatggtct gtttgggcag gtaaaattat gtaatgcagt gtttggaaca ggagaatttt
1381 ttttcctttt tatttcttta ttttttcttt tttactgtat aatgtccctc aagtttatgg
1441 cagtgtacct tgtgccactg aatttccaaa gtgtaccaat ttttttttt ttactgtgct
1501 tcaaataaat agaaaaatag ttataatatt gatcttcaac tttgccattc atgcttctat
```

```
1561 gcatattagg ctacgtattc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
1621 tatgccattt ctgggaaatg catctggagg ctaagtattg ctttctacaa ataattgccc
1681 cctttgtttt aaaaagaaga aatgcatatt gaagtagttt gatgatttgt ttggcatata
1741 ggaagcacgc tggtgctaag tatttttaa atggttatgt aagcaaagct gaactgtaaa
1801 tcttcaggaa tatgtattaa gattgtggaa tgggtgtaag acaattggta gggggtgaaa
1861 gtgggtttga ttaaatggat cttttatggc cctatgatct atcctttact tgaaagcttt
1921 tgaaaagtgg aaaggtcatt ttgttgcatt tccccatttc ttgtttttaa aagaccaaca
1981 aatctcaagc cctataaatg gcttgtattg aacccgaatt c
```

SEQ ID NO. 10

NP_000917
933 aa linear
progesterone receptor [Homo sapiens]

AAS00096
933 aa linear
progesterone receptor [Homo sapiens]

AAD01587
933 aa linear
progesterone receptor [Homo sapiens]

AAA60081
933 aa linear
progesterone receptor Homo sapiens

P06401
933 aa linear
Progesterone receptor (PR).

```
  1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdps dektqdqqsl sdvegaysra eatrgaggss ssppekdsgl ldsvldtlla
121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplm srsgc vgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedssese esagpllkgk
241 pralggaaag ggaaacppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesyd ggagaasafa pprtspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qqgpfapppc
481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggrkfk kfnkvrvvra ldavalpqpl
661 gvpnesqals qrftfspgqd iqlipplinl lmsiepdviy aghdntkpdt sssllтslnq
721 lgerqllsvv kwskslpgfr nlhiddqitl iqyswmslmv fglgwrsykh vsgqmlyfap
781 dlilneqrmk essfyslclt mwqipqefvk lqvsqeeflc mkvllllnti pleglrsqtq
841 feemrssyir elikaiglrq kgvvsssqrf yqltklldnl hdlvkqlhly clntfiqsra
901 lsvefpemms eviaaqlpki lagmvkpllf hkk
```

SEQ ID NO. 11

BAB91074
831 aa linear
delta 4 progesterone receptor [Homo sapiens]

```
  1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdps dektqdqqsl sdvegaysra eatrgaggss ssppekdsgl ldsvldtlla
121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qqgpfapppc
481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
661 lgwrsykhvs gqmlyfapdl ilneqrmkes sfyslcltmw qipqefvklq vsqeeflcmk
721 vllllntipl eglrsqtqfe emrssyirel ikaiglrqkg vvsssqrfyq ltklldnlhd
781 lvkqlhlycl ntfiqsrals vefpemmsev iaaqlpkila gmvkpllfhk k
```

SEQ ID NO. 12

BAC06585
695 aa linear
Progesterone receptor [Homo sapiens]

```
  1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdps dektqdqqsl sdvegaysra eatrgaggss ssppekdsgl ldsvldtlla
121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qqgpfapppc
481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
661 lgwrsykhvs gqmlyfapdl ilndsfgrat ksnpv
```

SEQ ID NO. 13

BAC11011
764 aa linear
delta 3+6/2 progesterone receptor [Homo sapiens].

```
  1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdps dektqdqqsl sdvegaysra eatrgaggss ssppekdsgl ldsvldtlla
121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qqgpfapppc
481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegrkf
601 kkfnkvrvvr aldavalpqp vgvpnesqal sqrftfspgq diqlipplin llmsiepdvi
661 yaghdntkpd tsssllltsln qlgerqllsv vkwskslpgf rnlhiddqit liqyswmslm
721 vfglgwrsyk hvsgqmlyfa pdlilneshr slssfklakk sssv
```

SEQ ID NO.14

BAC11012
690 aa linear
delta4+6/2 progesterone receptor [Homo sapiens]

```
  1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdps dektqdqqsl sdvegaysra eatrgaggss ssppekdsgl ldsvldtlla
121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qqgpfapppc
481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
661 lgwrsykhvs gqmlyfapdl ilneqsivts
```

SEQ ID NO.15

BAC11013
803 aa linear
delta 6/2 progesterone receptor [Homo sapiens].

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  1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
 61 prpcqgqdps dektqdqqsl sdvegaysra eatrgaggss ssppekdsgl ldsvldtlla
121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qqgpfapppc
481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggrkfk kfnkvrvvra ldavalpqpv
661 gvpnesqals qrftfspgqd iqlipplinl lmsiepdviy aghdntkpdt sssllltslnq
721 lgerqllsvv kwskslpgfr nlhiddqitl iqyswmslmv fglgwrsykh vsgqmlyfap
781 dlilneshrs lssfklakks ssv
```

SEQ ID NO. 16

FGQGGAGPVGGQGP

SEQ ID NO.17

CTGAGTC

SEQ ID NO. 18

YGEPGEVFINKGK

SEQ ID NO. 19

GIVEFASKPAAR

SEQ ID NO. 20

FAQHGTEEYEYSQR

SEQ ID NO. 21

NP_076092 (Murine PSF)

```
  1 msrdrfrsrg gggggfhrrg ggggrgglhd frspppgmgl nqnrgpmgpg pggpkpplpp
 61 ppphqqqqqp ppqqpppqqp pphqqppphq pphqqppppp qeskpvvpqg pgsapgvssa
121 pppavsappa nppttgappg pgptptpppa vpstapgppp pstpssgvst tppqtggppp
181 ppaggagpgp kpgpgpggpk ggkmpggpkp gggpgmgapg ghpkpphrgg geprggrqhh
241 apyhqqhhqg pppggpgprt eekisdsegf kanlsllrrp gektytqrcr lfvgnlpadi
301 tedefkrlfa kygepgevfi nkgkgfgfik lesralaeia kaelddtpmr grqlrvrfat
361 haaalsvrnl spyvsnelle eafsqfgpie ravvivddrg rstgkgivef askpaarkaf
421 ercsegvfll tttprpvive pleqlddedg lpeklaqknp myqkeretpp rfaqhgtfey
481 eysqrwksld emekqqreqv eknmkdakdk lesemedayh ehqanllrqd lmrrqeelrr
541 meelhsqemq krkemqlrqe eerrrreeem mirqremeeq mrrqreesys rmgymdprer
601 dmrmggggtm nmgdpygsgg qkfpplgggg gigyeanpgv ppatmsgsmm gsdmrterfg
661 qggagpvggq gprgmgpgtp agygrgreey egpnkkprf
```

SEQ ID NO. 22

VRMIDVG